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RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/10/041,574

TIME: 08:58:40

Input Set : N:\Crf3\RULE60\10041574.txt

Output Set: N:\CRF3\02082002\J041574.raw

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MAR 14 2002

TECH CENTER 1600/2900

ENTERED

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3 <110> APPLICANT: Ni, Jian
4     Yu, Guo-Liang
5     Fan, Ping
6     Gentz, Reiner L.
8 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
10 <130> FILE REFERENCE: PF375P1
12 <140> CURRENT APPLICATION NUMBER: 10/041,574
13 <141> CURRENT FILING DATE: 2002-01-10
15 <150> PRIOR APPLICATION NUMBER: 09/527,236
16 <151> PRIOR FILING DATE: 2000-03-16
18 <150> PRIOR APPLICATION NUMBER: 60/052,991
19 <151> PRIOR FILING DATE: 1997-06-11
21 <150> PRIOR APPLICATION NUMBER: 09/095,094
22 <151> PRIOR FILING DATE: 1998-06-10
24 <150> PRIOR APPLICATION NUMBER: 60/126,019
25 <151> PRIOR FILING DATE: 1999-03-24
27 <150> PRIOR APPLICATION NUMBER: 60/134,220
28 <151> PRIOR FILING DATE: 1999-05-14
30 <160> NUMBER OF SEQ ID NOS: 27
32 <170> SOFTWARE: PatentIn Ver. 2.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 3474
36 <212> TYPE: DNA
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56 ggggtgttgg aggtagatgg gctcccggcc cgaggaggcg cggtggatgc ggcgctgggc 180
58 agaagcagcc gccgattcca gctgccccgc gcgccccggg cgcccctgcg agtccccggt 240
60 tcagcc atg ggg acc tct ccg agc agc acc gcc ctc gcc tcc tgc 288
61     Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys
62     -40                               -35                               -30
64 agc cgc atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt 336
65 Ser Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu

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66      -25      -20      -15
68 ctc ctg ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag 384
69 Leu Leu Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys
70 -10      -5      -1 1      5
72 gcc tcg aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc 432
73 Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly
74      10      15      20
76 cag gtg cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag 480
77 Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu
78      25      30      35
80 cat tgt acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg 528
81 His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly
82      40      45      50
84 acc ttt acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt 576
85 Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser
86 55      60      65      70
88 cag cca tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg 624
89 Gln Pro Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu
90      75      80      85
92 act gac cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct 672
93 Thr Asp Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala
94      90      95      100
96 acc tgt gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag 720
97 Thr Cys Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys
98      105      110      115
100 aaa ggg aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt 768
101 Lys Gly Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly
102      120      125      130
104 acc ttc tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca 816
105 Thr Phe Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr
106 135      140      145      150
108 gac tgt ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag 864
109 Asp Cys Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu
110      155      160      165
112 aca gac aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca 912
113 Thr Asp Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser
114      170      175      180
116 cct tcc cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc 960
117 Pro Ser Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr
118      185      190      195
120 cat gaa gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca 1008
121 His Glu Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr
122      200      205      210
124 gaa tcc aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc 1056
125 Glu Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile
126 215      220      225      230
128 cag gaa ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa 1104
129 Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu
130      235      240      245

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132 gac gtg aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa 1152
133 Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln
134      250      255      260
136 ggc ccc cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc 1200
137 Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala
138      265      270      275
140 act ggg ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga 1248
141 Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly
142      280      285      290
144 cat cct aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg 1296
145 His Pro Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu
146 295      300      305      310
148 ccc tgg atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg 1344
149 Pro Trp Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val
150      315      320      325
152 gtg tgc agt atc cgg aaa agc tgc agg act ctg aaa aag ggg ccc cgg 1392
153 Val Cys Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg
154      330      335      340
156 cag gat ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg 1440
157 Gln Asp Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met
158      345      350      355
160 act cca acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat 1488
161 Thr Pro Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His
162      360      365      370
164 ggt atc gat atc ctg aag ctt gta gca gcc caa gtg gga agc cag tgg 1536
165 Gly Ile Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp
166 375      380      385      390
168 aaa gat atc tat cag ttt ctt tgc aat gcc agt gag agg gag gtt gct 1584
169 Lys Asp Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala
170      395      400      405
172 gct ttc tcc aat ggg tac aca gcc gac cac gag cgg gcc tac gca gct 1632
173 Ala Phe Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala
174      410      415      420
176 ctg cag cac tgg acc atc cgg ggc ccc gag gcc agc ctc gcc cag cta 1680
177 Leu Gln His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu
178      425      430      435
180 att agc gcc ctg cgc cag cac cgg aga aac gat gtt gtg gag aag att 1728
181 Ile Ser Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile
182      440      445      450
184 cgt ggg ctg atg gaa gac acc acc cag ctg gaa act gac aaa cta gct 1776
185 Arg Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala
186 455      460      465      470
188 ctc ccg atg agc ccc agc ccg ctt agc ccg agc ccc atc ccc agc ccc 1824
189 Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro
190      475      480      485
192 aac gcg aaa ctt gag aat tcc gct ctc ctg acg gtg gag cct tcc cca 1872
193 Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro
194      490      495      500
196 cag gac aag aac aag ggc ttc ttc gtg gat gag tcg gag ccc ctt ctc 1920

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197 Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu
198      505      510      515
200 cgc tgt gac tct aca tcc agc ggc tcc tcc gcg ctg agc agg aac ggt 1968
201 Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly
202      520      525      530
204 tcc ttt att acc aaa gaa aag aag gac aca gtg ttg cgg cag gta cgc 2016
205 Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg
206 535      540      545      550
208 ctg gac ccc tgt gac ttg cag cct atc ttt gat gac atg ctc cac ttt 2064
209 Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe
210      555      560      565
212 cta aat cct gag gag ctg cgg gtg att gaa gag att ccc cag gct gag 2112
213 Leu Asn Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu
214      570      575      580
216 gac aaa cta gac cgg cta ttc gaa att att gga gtc aag agc cag gaa 2160
217 Asp Lys Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu
218      585      590      595
220 gcc agc cag acc ctc ctg gac tct gtt tat agc cat ctt cct gac ctg 2208
221 Ala Ser Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu
222      600      605      610
224 ctg tagaactag ggatactgca ttctggaaat tactcaattt agtggcaggg 2261
225 Leu
226 615
228 tgggtttttta attttcttct gtttctgatt tttgttgttt ggggtgtgtg tgtgtgtttg 2321
230 tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tttacacagag aatatggcca 2381
232 gtgcttgagt tcttctcct tctctctctc tttttttttt aaataactct tctgggaagt 2441
234 tggtttataa gcctttgcca ggtgtaactg ttgtgaaata cccaccacta aagtttttta 2501
236 agttccatat tttctccatt ttgccttctt atgtattttc gagattattc tgtgcacttt 2561
238 aaatttactt aacttaccat aaatgcagtg tgacttttcc cacacactgg attgtgaggc 2621
240 tcttaacttc ttaaaaagtat aatggcatct tgtgaatcct ataagcagtc tttatgtctc 2681
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248 tgaccacact attgctgatt gtatggtttt cacctggaca ccgtgtagaa tgcttgatta 2921
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252 ggatttgcta tttaagtggc ttgacaactg ggccaccaa gaacttgaac ttcacctttt 3041
254 aggatttgag ctgttctgga acacattgct gcactttgga aagtcaaaat caagtgccag 3101
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258 atacacataa tcaataggtc caatctgctc tcaaggcctt ggtcctggtg ggattccttc 3221
260 accaattact ttaattaaaa atggctgcaa ctgtaagaac ccttgctctga tatatttgca 3281
262 actatgctcc catttacaaa tgtaccttct aatgctcagt tgccaggttc caatgcaaag 3341
264 gtggcgtgga ctccctttgt gtgggtgggg tttgtgggta gtggtgaagg accgatatca 3401
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272 <211> LENGTH: 655
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
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277 Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
278 -40 -35 -30 -25
280 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
281 -20 -15 -10
283 Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
284 -5 -1 1 5
286 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
287 10 15 20
289 Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
290 25 30 35 40
292 Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
293 45 50 55
295 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
296 60 65 70
298 Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
299 75 80 85
301 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
302 90 95 100
304 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
305 105 110 115 120
307 Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
308 125 130 135
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311 140 145 150
313 Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
314 155 160 165
316 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
317 170 175 180
319 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
320 185 190 195 200
322 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
323 205 210 215
325 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
326 220 225 230
328 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
329 235 240 245
331 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
332 250 255 260
334 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
335 265 270 275 280
337 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro
338 285 290 295
340 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp
341 300 305 310
343 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys
344 315 320 325
346 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp
347 330 335 340
349 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/041,574

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